

In the Specification

Please replace the paragraph at page 1, lines 3-8 with the following paragraph:

B¹ This application is a continuation-in-part of U.S. Patent Application No. 09/232,201 filed January 14, 1999, now U.S. Patent Number 6,348,321, which claims the benefit of U.S. Provisional Application No. 60/110,941 filed December 4, 1998; U.S. Provisional Application No. 60/093,491 filed July 20, 1998; and U.S. Provisional Application No. 60/071,374 filed January 15, 1998. The teachings of each of these referenced applications are incorporated herein by reference in their entirety.

Please replace the paragraph at page 32, lines 8 through 13 continuing to page 33, lines 1 through 16 with the following paragraph.

B² The comparison of sequences and determination of percent identity and similarity between two sequences can be accomplished using a mathematical algorithm. (*Computational Molecular Biology*, Lesk, A.M., ed., Oxford University Press, New York, 1988; *Biocomputing: Informatics and Genome Projects*, Smith, D.W., ed., Academic Press, New York, 1993; *Computer Analysis of Sequence Data, Part 1*, Griffin, A.M., and Griffin, H.G., eds., Humana Press, New Jersey, 1994; *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987; and *Sequence Analysis Primer*, Gribskov, M. and Devereaux, J., eds., M. Stockton Press, New York, 1991). In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available on the worldwide web at gcg.com), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (Devereux, J., et al., *Nucleic Acids Res.* 12(1):387 (1984)), using a NWSgapdna.CMP matrix and a gap weight of

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word. 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity between two amino acid or nucleotide sequences is determined using the algorithm of E. Meyers and W. Miller (*CABIOS*, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

Please replace the paragraph at page 33, lines 17 through 28 continuing to page 34, lines 1 through 2 with the following paragraph.

B³ The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (*J. Mol. Biol.* 215:403-10 (1990)). BLAST nucleotide searches can be performed with the NBLAST program, score = 100, word length = 12 to obtain nucleotide sequences homologous to (with calculatably significant similarity to) the nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, word length = 3 to obtain amino acid sequences homologous to the proteins of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (*Nucleic Acids Res.* 25(17):3389-3402 (1997)). When utilizing BLAST and gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. (see the worldwide web at ncbi.nlm.nih.gov)

Please replace the paragraph at page 34, lines 3 through 11 with the following paragraph.

B⁴ Similarity for nucleotide and amino acid sequences can be defined in terms of the parameters set by the Advanced Blast search available from NCBI (the National Center for Biotechnology Information. (see, for Advanced BLAST the worldwide web at ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast?Jform=1) These default parameters, recommended for a query molecule of length greater than 85 amino acid residues or nucleotides